SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: Studiengesellschaft Kohle mbH
(B) STREET: Kaiser-Wilhelm-Platz 1
(C) CITY: Muelheim an der Ruhr
(E) COUNTRY: Germany
(F) POSTAL CODE (ZIP): 45470

(ii) TITLE OF INVENTION: A Process for the Preperation and Identification of Novel Hydrolases Having Improved Properties

(iii) NUMBER OF SEQUENCES: 21

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCGCAATTAA CCCTCACTAA AGGGAACAAA 30

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCGTAATACG ACTCACTATA GGGCGAA 27

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:85..1017

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC    60

CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TAT CTG CTC CCC CTC       111
                           Met Lys Lys Lys Tyr Leu Leu Pro Leu
                           -26 -25                 -20

GGC CTG GCC ATC GGT CTC GCC GCT CTC GCT GCC AGC CCT CTG ATC CAG      159
Gly Leu Ala Ile Gly Leu Ala Ala Leu Ala Ala Ser Pro Leu Ile Gln
    -15                 -10                 -5

GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC      207
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
  1               5                  10                  15

ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT      255
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
             20                  25                  30

CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC      303
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val
         35                  40                  45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG      351
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
     50                  55                  60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC      399
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
 65                  70                  75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT      447
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
 80                  85                  90                  95

CCC GAC CTG ATC GCT TCC GCC ATC AGC GTC GGC GCC CCG CAC AAG GGT      495
Pro Asp Leu Ile Ala Ser Ala Ile Ser Val Gly Ala Pro His Lys Gly
                100                 105                 110

TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC      543
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
            115                 120                 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC      591
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
        130                 135                 140
```

```
TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG     639
Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu
    145                 150                 155

GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG     687
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
160                 165                 170                 175

CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC     735
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
                180                 185                 190

GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC     783
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
            195                 200                 205

CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG     831
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys
        210                 215                 220

AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG     879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu
    225                 230                 235

GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG     927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val
240                 245                 250                 255

AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC     975
Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser
                260                 265                 270

GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG             1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu
            275                 280                 285

TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC                                1049
```

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Met Lys Lys Lys Tyr Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala
-26 -25                 -20                 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr
-10                  -5                   1                   5

Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile
                10                  15                  20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp
            25                  30                  35
```

```
Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu
     40                  45                  50

Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu
 55                  60                  65                  70

Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro
                 75                  80                  85

Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala
             90                  95                 100

Ile Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu
        105                 110                 115

Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu
    120                 125                 130

Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr
135                 140                 145                 150

Gly Thr Gln Asn Ser Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly
                155                 160                 165

Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala
            170                 175                 180

Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp
        185                 190                 195

Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe
    200                 205                 210

Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly
215                 220                 225                 230

Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn
                235                 240                 245

Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr
            250                 255                 260

Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn
        265                 270                 275

Arg Leu Lys Asn Ala Ser Leu
    280                 285
```

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:85..1017

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC    60

CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC      111
                               Met Lys Lys Lys Ser Leu Leu Pro Leu
                              -26 -25                 -20

GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG     159
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
        -15                 -10                 -5

GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC     207
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
      1               5                  10                  15

ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT     255
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
                  20                  25                  30

CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC     303
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val
              35                  40                  45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG     351
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
          50                  55                  60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC     399
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
      65                  70                  75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT     447
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
 80                  85                  90                  95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT     495
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly
                100                 105                 110

TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC     543
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
            115                 120                 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC     591
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
        130                 135                 140

TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG     639
Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu
    145                 150                 155

GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG     687
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
160                 165                 170                 175
```

```
CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC     735
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
                180                 185                 190

GGC GTG AGC TAT TAC TGC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC     783
Gly Val Ser Tyr Tyr Cys Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
            195                 200                 205

CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG     831
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys
        210                 215                 220

AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG     879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu
    225                 230                 235

GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG     927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val
240                 245                 250                 255

AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC     975
Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser
                260                 265                 270

GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG             1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu
            275                 280                 285

TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC                                1049
```

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala
-26 -25                 -20                 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr
-10                  -5                   1                   5

Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile
             10                  15                  20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp
         25                  30                  35

Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu
     40                  45                  50

Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu
 55                  60                  65                  70

Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro
                 75                  80                  85
```

```
Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala
                90                  95                  100

Thr Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu
        105                 110                 115

Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu
    120                 125                 130

Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr
135                 140                 145                 150

Gly Thr Gln Asn Ser Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly
                155                 160                 165

Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala
            170                 175                 180

Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp
        185                 190                 195

Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe
    200                 205                 210

Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly
215                 220                 225                 230

Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn
                235                 240                 245

Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr
            250                 255                 260

Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn
        265                 270                 275

Arg Leu Lys Asn Ala Ser Leu
    280                 285
```

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:85..1017

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC   60
```

```
CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC      111
                           Met Lys Lys Lys Ser Leu Leu Pro Leu
                          -26 -25                  -20

GGC CTG GCC ATC GGT CTG GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG      159
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
        -15                 -10                  -5

GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC      207
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
      1               5                  10                  15

ATG CTC GGC TTC GAC AAC ATC CTT GGG GTC GAC TAC TGG TTC GGC ATT      255
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
                20                  25                  30

CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC      303
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val
            35                  40                  45

AGC CAG TTG GAC ACC TCG GAA GTA CGC GGC GAG CAG TTG CTG CAA CAG      351
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
        50                  55                  60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC      399
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
    65                  70                  75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT      447
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
 80                  85                  90                  95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT      495
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly
                100                 105                 110

TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC      543
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
            115                 120                 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC      591
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
        130                 135                 140

TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TTA CTG GGC TCG CTG      639
Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Leu Leu Gly Ser Leu
    145                 150                 155

GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG      687
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
160                 165                 170                 175

CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC      735
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
                180                 185                 190

GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC      783
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
            195                 200                 205
```

```
CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG     831
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys
            210                 215                 220

AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG     879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu
    225                 230                 235

GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG     927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val
240                 245                 250                 255

AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC     975
Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser
                260                 265                 270

GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG             1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu
            275                 280                 285

TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC                                1049
```

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```
Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala
-26 -25                 -20                 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr
-10                  -5                   1                   5

Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile
                10                  15                  20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp
            25                  30                  35

Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu
        40                  45                  50

Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu
    55                  60                  65                  70

Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro
                75                  80                  85

Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala
            90                  95                  100

Thr Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu
        105                 110                 115

Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu
    120                 125                 130
```

```
Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr
135                 140                 145                 150

Gly Thr Gln Asn Leu Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly
                155                 160                 165

Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala
            170                 175                 180

Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp
        185                 190                 195

Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe
    200                 205                 210

Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly
215                 220                 225                 230

Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn
                235                 240                 245

Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr
            250                 255                 260

Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn
        265                 270                 275

Arg Leu Lys Asn Ala Ser Leu
    280                 285


(2) INFORMATION FOR SEQ ID NO: 9:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1047 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: unknown
            (D) TOPOLOGY: unknown

     (ii) MOLECULE TYPE: DNA (genomic)

     (ix) FEATURE:
            (A) NAME/KEY: CDS
            (B) LOCATION:84..1016

     (ix) FEATURE:
            (A) NAME/KEY: mat_peptide
            (B) LOCATION:162..1016

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGATCCCCGG TTCTCCCGGA AGGATTCGGG CGATGGCTGG CAGGACGCGC CCCTCGGCCC   60

CATCAACCTG AGATGAGAAC AAC ATG AAG AAG AAG TCT CTG CTC CCC CTC       110
                          Met Lys Lys Lys Ser Leu Leu Pro Leu
                          -26 -25                 -20

GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG     158
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
        -15                 -10                  -5
```

```
GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC     206
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
  1               5                  10                  15

ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT     254
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
            20                  25                  30

CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC     302
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val
        35                  40                  45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG     350
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
    50                  55                  60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC     398
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
65                  70                  75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT     446
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
 80                  85                  90                  95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT     494
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly
            100                 105                 110

TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC     542
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
        115                 120                 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC     590
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
    130                 135                 140

TTC CTT TCC AGC GGC AGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG     638
Phe Leu Ser Ser Gly Ser Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu
145                 150                 155

GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG     686
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
160                 165                 170                 175

CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC     734
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
            180                 185                 190

GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC     782
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
        195                 200                 205

CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG     830
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys
    210                 215                 220

AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG     878
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu
225                 230                 235
```

```
GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG     926
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val
240                 245                 250                 255

AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC     974
Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser
                260                 265                 270

GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG             1016
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu
            275                 280                 285

TAGGACCCCG GCCGGGGCCT CGGCCCGGGC C                                 1047
```

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
Met Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala
-26 -25                 -20                 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr
-10                  -5                   1                   5

Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile
                10                  15                  20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp
            25                  30                  35

Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu
        40                  45                  50

Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu
 55                  60                  65                  70

Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro
                75                  80                  85

Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala
            90                  95                  100

Thr Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu
        105                 110                 115

Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu
    120                 125                 130

Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Ser Thr
135                 140                 145                 150

Gly Thr Gln Asn Ser Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly
                155                 160                 165
```

```
Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala
            170                 175                 180

Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp
        185                 190                 195

Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe
    200                 205                 210

Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly
215                 220                 225                 230

Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn
                235                 240                 245

Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr
            250                 255                 260

Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn
        265                 270                 275

Arg Leu Lys Asn Ala Ser Leu
    280                 285
```

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:85..1017

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC    60

CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC       111
                           Met Lys Lys Lys Ser Leu Leu Pro Leu
                          -26 -25                 -20

GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG     159
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
        -15                 -10                 -5

GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC     207
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
    1               5                  10                  15

ATG CTC GGC TTC GAC AAC ATC CTT GGG GTC GAC TAC TGG TTC GGC ATT     255
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
                20                  25                  30
```

```
CCC AGC GCC TTG GGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GGC     303
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Gly
            35                  40                  45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG     351
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
        50                  55                  60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC     399
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
    65                  70                  75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT     447
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
 80                  85                  90                  95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT     495
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly
                100                 105                 110

TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC     543
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
            115                 120                 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC     591
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
        130                 135                 140

TTC CTT TCC AGC GGC GGC ACC GGT ACC CAG AAT TTA CTG GGC TCG CTG     639
Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Leu Leu Gly Ser Leu
    145                 150                 155

GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG     687
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
160                 165                 170                 175

CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC     735
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
                180                 185                 190

GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC     783
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
            195                 200                 205

CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG     831
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys
        210                 215                 220

AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG     879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu
    225                 230                 235

GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG     927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val
240                 245                 250                 255

AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC     975
Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser
                260                 265                 270
```

```
GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG                1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu
            275                 280                 285

TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC                                   1049
```

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala
-26 -25                 -20                 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr
-10                  -5                   1                   5

Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile
             10                  15                  20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp
         25                  30                  35

Gly Ala Gln Val Tyr Val Thr Glu Gly Ser Gln Leu Asp Thr Ser Glu
     40                  45                  50

Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu
 55                  60                  65                  70

Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro
                 75                  80                  85

Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala
             90                  95                 100

Thr Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu
        105                 110                 115

Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu
    120                 125                 130

Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr
135                 140                 145                 150

Gly Thr Gln Asn Leu Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly
                155                 160                 165

Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala
            170                 175                 180

Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp
        185                 190                 195

Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe
    200                 205                 210
```

```
Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly
215                 220                 225                 230

Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn
                235                 240                 245

Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr
            250                 255                 260

Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn
        265                 270                 275

Arg Leu Lys Asn Ala Ser Leu
    280                 285
```

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1050 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:85..1017

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```
GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC   60

CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC      111
                           Met Lys Lys Lys Ser Leu Leu Pro Leu
                          -26 -25                 -20

GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG     159
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
        -15                 -10                 -5

GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC     207
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
  1               5                  10                  15

ATG CTC GGC TTC GAC AAC ATC CTT GGG GTC GAC TAC TGG TTC GGC ATT     255
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
            20                  25                  30

CCC AAC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GGC     303
Pro Asn Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Gly
        35                  40                  45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG     351
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
    50                  55                  60
```

```
GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC     399
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
      65                  70                  75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT     447
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
 80                  85                  90                  95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT     495
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly
                100                 105                 110

TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC     543
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
            115                 120                 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC     591
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
        130                 135                 140

TTC CTT TCC AGC GGC GGC ACC GGT GCG CAG AAT TTA CTG GGC TCG CTG     639
Phe Leu Ser Ser Gly Gly Thr Gly Ala Gln Asn Leu Leu Gly Ser Leu
    145                 150                 155

GAG TCG CTG AAC AGC GAG GGT GCC GGC CGC TTC AAC GCC AAG TAC CCG     687
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
160                 165                 170                 175

CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCT TAC AAG GTC AAC     735
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
                180                 185                 190

GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC     783
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
            195                 200                 205

CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG     831
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys
        210                 215                 220

AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG     879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu
    225                 230                 235

GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG     927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val
240                 245                 250                 255

AAC CAG GTC CTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC     975
Asn Gln Val Leu Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser
                260                 265                 270

GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG             1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu
            275                 280                 285

TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CCG                               1050
```

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala
-26 -25                 -20                 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr
-10                  -5                   1                   5

Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile
                10                  15                  20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Asn Ala Leu Arg Arg Asp
            25                  30                  35

Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu
        40                  45                  50

Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu
 55                  60                  65                  70

Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro
                75                  80                  85

Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala
            90                  95                 100

Thr Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu
        105                 110                 115

Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu
    120                 125                 130

Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr
135                 140                 145                 150

Gly Thr Gln Asn Leu Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly
                155                 160                 165

Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala
            170                 175                 180

Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp
        185                 190                 195

Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe
    200                 205                 210

Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly
215                 220                 225                 230

Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn
                235                 240                 245
```

```
Tyr Arg Met Asp His Leu Asp Glu Val Asn Gln Val Leu Gly Leu Thr
            250                 255                 260

Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn
        265                 270                 275

Arg Leu Lys Asn Ala Ser Leu
    280                 285
```

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:85..1017

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```
GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC   60

CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC      111
                              Met Lys Lys Lys Ser Leu Leu Pro Leu
                             -26 -25                 -20

GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG     159
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
        -15                 -10                 -5

GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC     207
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
    1               5                  10                  15

ATG CTC GGC TTC GAC AAC ATC CTT GGG GTC GAC TAC TGG TTC GGC ATT     255
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
                20                  25                  30

CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GGC     303
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Gly
            35                  40                  45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG     351
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
        50                  55                  60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC     399
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
    65                  70                  75
```

```
GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT     447
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
 80                  85                  90                  95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AGG GGT     495
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Arg Gly
                100                 105                 110

TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC     543
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
            115                 120                 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC     591
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
        130                 135                 140

TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TTA CTG GGC TCG CTG     639
Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Leu Leu Gly Ser Leu
    145                 150                 155

GAG TCG CTG AAC AGT GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG     687
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
160                 165                 170                 175

CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCT TAC AAG GTC AAC     735
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
                180                 185                 190

GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC     783
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
            195                 200                 205

CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG     831
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys
        210                 215                 220

AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG     879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu
    225                 230                 235

GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG     927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val
240                 245                 250                 255

AAC CAG GTC CTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC     975
Asn Gln Val Leu Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser
                260                 265                 270

GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG            1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu
            275                 280                 285

TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC                               1049
```

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```
Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala
-26 -25                 -20                 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr
-10                  -5                   1                   5

Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile
              10                  15                  20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp
          25                  30                  35

Gly Ala Gln Val Tyr Val Thr Glu Gly Ser Gln Leu Asp Thr Ser Glu
      40                  45                  50

Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu
 55                  60                  65                  70

Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro
                 75                  80                  85

Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala
             90                  95                 100

Thr Ser Val Gly Ala Pro His Arg Gly Ser Asp Thr Ala Asp Phe Leu
        105                 110                 115

Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu
    120                 125                 130

Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr
135                 140                 145                 150

Gly Thr Gln Asn Leu Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly
                155                 160                 165

Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala
            170                 175                 180

Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp
        185                 190                 195

Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe
    200                 205                 210

Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly
215                 220                 225                 230

Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn
                235                 240                 245

Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Leu Gly Leu Thr
            250                 255                 260

Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn
        265                 270                 275

Arg Leu Lys Asn Ala Ser Leu
    280                 285
```

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:85..1017

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:163..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```
GGATCCCCCG GTTCTCCCGG AAGGATTGGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC    60

CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC       111
                           Met Lys Lys Lys Ser Leu Leu Pro Leu
                          -26 -25                 -20

GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG      159
Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
        -15                 -10                 -5

GCC AGC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC      207
Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
      1               5                  10                  15

ATG CTC GGC TTC GAC AAC ATC CTT GGG GTC GAC TAC TGG TTC GGC ATT      255
Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
                   20                  25                  30

CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GGC      303
Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Gly
               35                  40                  45

AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG      351
Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
           50                  55                  60

GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC      399
Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
       65                  70                  75

GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT      447
Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
 80                  85                  90                  95

CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT      495
Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly
                  100                 105                 110
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TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC     543
Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
            115                 120                 125

GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC     591
Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
        130                 135                 140

TTC CTT TCC AGC GGC GGC ATC GGT ACG CAG AAT TTT CTG GGC TCG CTG     639
Phe Leu Ser Ser Gly Gly Ile Gly Thr Gln Asn Phe Leu Gly Ser Leu
    145                 150                 155

GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG     687
Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
160                 165                 170                 175

CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC     735
Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
                180                 185                 190

GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC     783
Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
            195                 200                 205

CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG     831
Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys
        210                 215                 220

AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG     879
Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu
    225                 230                 235

GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG     927
Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val
240                 245                 250                 255

AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC     975
Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser
                260                 265                 270

GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG             1017
Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu
            275                 280                 285

TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC                                1049


(2) INFORMATION FOR SEQ ID NO: 18:

       (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 311 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Lys Lys Lys Ser Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala
-26 -25                 -20                 -15

Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr
-10                  -5                   1                   5
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Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile
                10                  15                  20

Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp
            25                  30                  35

Gly Ala Gln Val Tyr Val Thr Glu Gly Ser Gln Leu Asp Thr Ser Glu
        40                  45                  50

Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Glu Ile Val Ala Leu
 55                  60                  65                  70

Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro
                75                  80                  85

Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala
            90                  95                  100

Thr Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu
        105                 110                 115

Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu
    120                 125                 130

Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Ile
135                 140                 145                 150

Gly Thr Gln Asn Phe Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly
                155                 160                 165

Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala
            170                 175                 180

Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp
        185                 190                 195

Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe
    200                 205                 210

Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly
215                 220                 225                 230

Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn
                235                 240                 245

Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr
            250                 255                 260

Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn
        265                 270                 275

Arg Leu Lys Asn Ala Ser Leu
    280                 285
```

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCGCAATTAA CCCTCACTAA AGGGAACAAA 30

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GGTACGCAGA ATNNNCTGGG CTCGC 25

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCGTAATACG ACTCACTATA GGGCGAA 27